



results of **BLAST**

BLASTN 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1005939809-15110-323

Query=

(40 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).;
1,020,477 sequences; 4,355,661,355 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 54 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score	E
(bits)	Value

<u>gi 7706766 ref NM 016113.1 </u>	Homo sapiens vanilloid receptor...	66	1e-09
<u>gi 5305597 gb AF103906.1 AF103906</u>	Homo sapiens vanilloid re...	66	1e-09
<u>gi 10184146 emb AX023795.1 AX023795</u>	Sequence 1 from Patent ...	66	1e-09
<u>gi 7023447 dbj AK001896.1 AK001896</u>	Homo sapiens cDNA FLJ110...	58	4e-07
<u>gi 15281201 gb AC010608.7 </u>	Homo sapiens chromosome 5 clone ...	38	0.33
<u>gi 15451689 gb AC025464.5 </u>	Homo sapiens chromosome 5 clone ...	38	0.33
<u>gi 6651379 gb AF172277.1 AF172277</u>	Homo sapiens 7q21 clones ...	38	0.33
<u>gi 11120966 gb AC007567.2 AC007567</u>	Homo sapiens BAC clone C...	38	0.33
<u>gi 15807672</u>	Unknown	36	1.3
<u>gi 15638817 gb AC080073.6 </u>	Homo sapiens chromosome 7 clone ...	36	1.3
<u>gi 6460468 gb AE001862.1 AE001862</u>	Deinococcus radiodurans R...	36	1.3
<u>gi 5042401 gb AC007786.1 AC007786</u>	Homo sapiens chromosome 1...	36	1.3
<u>gi 6689159 emb AL136058.1 SCE20</u>	Streptomyces coelicolor cos...	36	1.3
<u>gi 3253129 gb AC004223.1 AC004223</u>	Homo sapiens chromosome 1...	36	1.3
<u>gi 298270 gb S55307.1 S55307</u>	ATP nucleotide 3'-pyrophosphok...	36	1.3
<u>gi 13470324</u>	Unknown	34	5.2
<u>gi 15805042</u>	Unknown	34	5.2
<u>gi 15144462 gb AC012500.7 </u>	Homo sapiens BAC clone RP11-434M...	34	5.2
<u>gi 16596540 gb AC092365.3 </u>	Homo sapiens chromosome 16 clone...	34	5.2
<u>gi 16195215 gb AC022103.5 </u>	Homo sapiens chromosome 5 clone ...	34	5.2
<u>gi 15451661 gb AC010458.6 </u>	Homo sapiens chromosome 19 clone...	34	5.2
<u>gi 13096815 gb BC003201.1 BC003201</u>	Mus musculus, chondroiti...	34	5.2
<u>gi 14150415 gb AC012476.8 AC012476</u>	Homo sapiens chromosome ...	34	5.2
<u>gi 10946955 ref NM 021528.1 </u>	Mus musculus chondroitin 4-sul...	34	5.2
<u>gi 2588621 gb AC003084.1 AC003084</u>	Human BAC clone CTB-84D4 ...	34	5.2
<u>gi 3417290 gb U95737.1 HUU95737</u>	Human Chromosome 16 BAC clo...	34	5.2
<u>gi 4809180 gb AF136344.1 AF136344</u>	Toxoplasma gondii catalas...	34	5.2
<u>gi 3900858 gb AC004848.1 AC004848</u>	Homo sapiens PAC clone RP...	34	5.2
<u>gi 6458057 gb AE001898.1 AE001898</u>	Deinococcus radiodurans R...	34	5.2
<u>gi 15881473 emb AJ337055.1 HSA337055</u>	Homo sapiens genomic s...	34	5.2
<u>gi 15880290 emb AJ335872.1 HSA335872</u>	Homo sapiens genomic s...	34	5.2
<u>gi 15878939 emb AJ334521.1 HSA334521</u>	Homo sapiens genomic s...	34	5.2
<u>gi 15870433 emb AJ326039.1 HSA326039</u>	Homo sapiens genomic s...	34	5.2
<u>gi 5579391 gb AF161267.1 AF161267</u>	Toxoplasma gondii catalas...	34	5.2
<u>gi 14715658 emb AL161651.13 AL161651</u>	Human DNA sequence fro...	34	5.2
<u>gi 14041741 emb AL133351.33 AL133351</u>	Human DNA sequence fro...	34	5.2
<u>gi 10178502 emb AL355392.7 AL355392</u>	Human DNA sequence from...	34	5.2
<u>gi 13445335 emb AL161779.32 AL161779</u>	Human DNA sequence fro...	34	5.2
<u>gi 10944277 emb AL121753.30 HSDJ61404</u>	Human DNA sequence fr...	34	5.2
<u>gi 13274200 emb AL122008.28 HSJ799P18</u>	Human DNA sequence fr...	34	5.2
<u>gi 9408716 emb AL121980.14 HS1007G16</u>	Human DNA sequence fro...	34	5.2
<u>gi 3366580 gb AC004049.1 AC004049</u>	Homo sapiens chromosome 4...	34	5.2
<u>gi 7228177 emb AL133215.16 AL133215</u>	Human DNA sequence from...	34	5.2
<u>gi 57236 emb X16362.1 RNSERPG</u>	Rat SPI-2 serine protease inh...	34	5.2
<u>gi 8017427 emb AJ289132.1 MMU289132</u>	Mus musculus mRNA for c...	34	5.2
<u>gi 5420383 emb AL034384.1 HSMTM0</u>	Human chromosome Xq28, cos...	34	5.2
<u>gi 1698996 gb U78190.1 HSU78190</u>	Human GTP cyclohydrolase I ...	34	5.2
<u>gi 16549752 dbj AK055096.1 AK055096</u>	Homo sapiens cDNA FLJ30...	34	5.2
<u>gi 14588673 dbj AP003492.2 AP003492</u>	Oryza sativa genomic DN...	34	5.2
<u>gi 14023393 dbj AP003001.2 AP003001</u>	Mesorhizobium loti DNA,...	34	5.2
<u>gi 205037 gb M67496.1 RATKBP</u>	Rat kallikrein-binding protein...	34	5.2
<u>gi 13488765 dbj AP000802.4 AP000802</u>	Homo sapiens genomic DN...	34	5.2
<u>gi 13429916 dbj AP001922.4 AP001922</u>	Homo sapiens genomic DN...	34	5.2
<u>gi 12381920 dbj AP002815.3 AP002815</u>	Homo sapiens genomic DN...	34	5.2

Alignments

>gi|7706766|ref|NM 016113.1| Homo sapiens vanilloid receptor-like protein (VRL), mRNA

Length = 2507

Score = 65.9 bits (33), Expect = 1e-09
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||
Sbjct: 77 ccgacgcgcagctgggaggaagacaggaccctt 109

>gi|5305597|gb|AF103906.1|AF103906 Homo sapiens vanilloid receptor-like protein (VRL
cds
Length = 2507

Score = 65.9 bits (33), Expect = 1e-09
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||
Sbjct: 77 ccgacgcgcagctgggaggaagacaggaccctt 109

>gi|10184146|emb|AX023795.1|AX023795 Sequence 1 from Patent WO0022121
Length = 2765

Score = 65.9 bits (33), Expect = 1e-09
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||
Sbjct: 269 ccgacgcgcagctgggaggaagacaggaccctt 301

>gi|7023447|dbj|AK001896.1|AK001896 Homo sapiens cDNA FLJ11034 fis, clone PLACE10042
Length = 2126

Score = 58.0 bits (29), Expect = 4e-07
Identities = 32/33 (96%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||
Sbjct: 241 ccgacgcgcagctgggaggaagacaggaccctt 273

>gi|15281201|gb|AC010608.7| Homo sapiens chromosome 5 clone CTB-3M24, complete seque
Length = 210408

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagacag 33
|||||
Sbjct: 97477 gcagctgggaggaagacag 97495

>gi|15451689|gb|AC025464.5| Homo sapiens chromosome 5 clone CTD-2260C5, complete seq
Length = 115265

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%)

Strand = Plus / Minus

Query: 15 gcagctgggaggaagacag 33
|||||||
Sbjct: 81325 gcagctgggaggaagacag 81307

>gi|6651379|gb|AF172277.1|AF172277 Homo sapiens 7q21 clones 267017 and 256L2 including genes, complete sequence
Length = 227054

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagacag 33
|||||||
Sbjct: 40139 gcagctgggaggaagacag 40157

>gi|11120966|gb|AC007567.2|AC007567 Homo sapiens BAC clone CTB-36G2 from 7q31, complete sequence
Length = 187413

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 15 gcagctgggaggaagacag 33
|||||||
Sbjct: 43518 gcagctgggaggaagacag 43500

Score = 36.2 bits (18), Expect = 1.3
Identities = 0/18 (0%)
Strand = Plus / Minus

Query: 2 acgaggccgacgcgcagc 19
|||||||

>gi|15638817|gb|AC080073.6| Homo sapiens chromosome 7 clone RP11-321C7, complete sequence
Length = 57075

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 17 agctgggaggaagacagg 34
|||||||
Sbjct: 36773 agctgggaggaagacagg 36790

>gi|6460468|gb|AE001862.1|AE001862 Deinococcus radiodurans R1 section 1 of 2 of the genome
Length = 213732

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 2 acgaggccgacgcgcagc 19
|||||||
Sbjct: 208524 acgaggccgacgcgcagc 208507

>gi|5042401|gb|AC007786.1|AC007786 Homo sapiens chromosome 19, BAC 41855 (CIT-B-3204)
Length = 100000

Length = 229061

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 20 tgggaggaagacaggacc 37
|||||||
Sbjct: 175566 tgggaggaagacaggacc 175583

>gi|6689159|emb|AL136058.1|SCE20 Streptomyces coelicolor cosmid E20
Length = 33820

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 2 acgaggccgacgcgcagc 19
|||||||
Sbjct: 18706 acgaggccgacgcgcagc 18689

>gi|3253129|gb|AC004223.1|AC004223 Homo sapiens chromosome 17, clone HRPC837J1, comp
Length = 101328

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 21 gggaggaagacaggaccc 38
|||||||
Sbjct: 78669 gggaggaagacaggaccc 78652

>gi|298270|gb|S55307.1|S55307 ATP nucleotide 3'-pyrophosphokinase [Streptomyces moro
Genomic, 1116 nt]
Length = 1116

Score = 36.2 bits (18), Expect = 1.3
Identities = 21/22 (95%)
Strand = Plus / Minus

Query: 1 cacgaggccgacgcgcagctgg 22
||||||| |||||
Sbjct: 1110 cacgaggccgacgcgcagctgg 1089

Score = 34.2 bits (17), Expect = 5.2
Identities = 0/17 (0%)
Strand = Plus / Minus

Query: 3 cgaggccgacgcgcagc 19

Score = 34.2 bits (17), Expect = 5.2
Identities = 0/17 (0%)
Strand = Plus / Minus

Query: 2 acgaggccgacgcgcag 18

>gi|15144462|gb|AC012500.7| Homo sapiens BAC clone RP11-434M17 from 2, complete sequ

Length = 117763

Score = 34.2 bits (17), Expect = 5.2
Identities = 23/25 (92%)
Strand = Plus / Minus

Query: 15 gcagctgggaggaagacaggaccct 39
|||||||
Sbjct: 111985 gcagctgggaggaagacaggaccct 111961

>gi|16596540|gb|AC092365.3| Homo sapiens chromosome 16 clone RP11-450B4, complete se
Length = 181329

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 19 ctgggaggaagacagga 35
|||||||
Sbjct: 14707 ctgggaggaagacagga 14691

>gi|16195215|gb|AC022103.5| Homo sapiens chromosome 5 clone CTC-254B4, complete sequ
Length = 129175

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 17 agctgggaggaagacag 33
|||||||
Sbjct: 123247 agctgggaggaagacag 123263

>gi|15451661|gb|AC010458.6| Homo sapiens chromosome 19 clone CTD-2265M8, complete se
Length = 105788

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 16 cagctgggaggaagaca 32
|||||||
Sbjct: 98762 cagctgggaggaagaca 98746

>gi|13096815|gb|BC003201.1|BC003201 Mus musculus, chondroitin 4-sulfotransferase 2,
IMAGE:3586766, mRNA, complete cds
Length = 1785

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagac 31
|||||||
Sbjct: 1284 gcagctgggaggaagac 1300

>gi|14150415|gb|AC012476.8|AC012476 Homo sapiens chromosome 15 clone RP11-532F12 map
sequence
Length = 178248

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 9 cgacgcgcagctgggag 25
|||||
Sbjct: 77450 cgacgcgcagctgggag 77434

>gi|10946955|ref|NM_021528.1| Mus musculus chondroitin 4-sulfotransferase 2 (C4st2-p
Length = 1715

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagac 31
|||||
Sbjct: 1216 gcagctgggaggaagac 1232

>gi|2588621|gb|AC003084.1|AC003084 Human BAC clone CTB-84D4 from 7q31, complete sequ
Length = 166219

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 21 gggaggaagacaggacc 37
|||||
Sbjct: 150301 gggaggaagacaggacc 150285

>gi|3417290|gb|U95737.1|HUU95737 Human Chromosome 16 BAC clone CIT987SK-A-388D4, com
sapiens]
Length = 93431

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 19 ctgggaggaagacagga 35
|||||
Sbjct: 17754 ctgggaggaagacagga 17770

>gi|4809180|gb|AF136344.1|AF136344 Toxoplasma gondii catalase mRNA, complete cds
Length = 2448

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 24 aggaagacaggaccctt 40
|||||
Sbjct: 1730 aggaagacaggaccctt 1746

>gi|3900858|gb|AC004848.1|AC004848 Homo sapiens PAC clone RP4-649P17 from 7q11.23-q2
Length = 135214

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 24 aggaagacaggaccctt 40
 |||||
 Sbjct: 104601 aggaagacaggaccctt 104617

>gi|6458057|gb|AE001898.1|AE001898 Deinococcus radiodurans R1 section 35 of 229 of t
 chromosome 1
 Length = 12523

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Minus

Query: 2 acgaggccgacgcgcag 18
 |||||
 Sbjct: 6963 acgaggccgacgcgcag 6947

>gi|15881473|emb|AJ337055.1|HSA337055 Homo sapiens genomic sequence surrounding NotI
 Length = 780

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Plus

Query: 21 gggaggaagacaggacc 37
 |||||
 Sbjct: 657 gggaggaagacaggacc 673

>gi|15880290|emb|AJ335872.1|HSA335872 Homo sapiens genomic sequence surrounding NotI
 Length = 731

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34
 |||||
 Sbjct: 201 gctgggaggaagacagg 185

>gi|15878939|emb|AJ334521.1|HSA334521 Homo sapiens genomic sequence surrounding NotI
 NL1-FH17R
 Length = 748

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34
 |||||
 Sbjct: 201 gctgggaggaagacagg 185

>gi|15870433|emb|AJ326039.1|HSA326039 Homo sapiens genomic sequence surrounding NotI
 NL1-DF17C
 Length = 609

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34
 |||||

Sbjct: 201 gctgggaggaagacagg 185

>gi|5579391|gb|AF161267.1|AF161267 Toxoplasma gondii catalase gene, complete cds
Length = 6957

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 24 aggaagacaggaccctt 40
|||||
Sbjct: 6423 aggaagacaggaccctt 6439

>gi|14715658|emb|AL161651.13|AL161651 Human DNA sequence from clone RP11-449I17 on c
sequence [Homo sapiens]
Length = 211627

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 23 gaggaagacaggaccct 39
|||||
Sbjct: 183591 gaggaagacaggaccct 183575

>gi|14041741|emb|AL133351.33|AL133351 Human DNA sequence from clone RP1-90J20 on chr
complete sequence [Homo sapiens]
Length = 167569

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 13 gcgcagctgggaggaag 29
|||||
Sbjct: 118916 gcgcagctgggaggaag 118900

>gi|10178502|emb|AL355392.7|AL355392 Human DNA sequence from clone RP5-1187J4 on chr
Contains ESTs, STSSs, GSSs and two CpG islands. Contains the
gene for novel protein similar to mouse von Ebner salivary
gland protein, the gene for a novel protein similar to rat
RYF3,>
Length = 159440

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 21 gggaggaagacaggacc 37
|||||
Sbjct: 126470 gggaggaagacaggacc 126454

>gi|13445335|emb|AL161779.32|AL161779 Human DNA sequence from clone RP6-29D12 on chr
complete sequence [Homo sapiens]
Length = 102528

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 15 gcagctgggaggaagac 31
 |||||
 Sbjct: 16780 gcagctgggaggaagac 16764

>[gi|10944277|emb|AL121753.30|HSDJ61404](#) Human DNA sequence from clone RP4-61404 on ch
 Contains the 3' part of the MMP24 gene for matrix
 metalloproteinase 24 (membrane-inserted), the ITGB4BP gene
 for integrin beta 4 binding protein, a novel gene similar
 to a metalloproteinase
 Length = 150481

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Minus

Query: 19 ctgggaggaagacagga 35
 |||||
 Sbjct: 79093 ctgggaggaagacagga 79077

>[gi|13274200|emb|AL122008.28|HSJ799P18](#) Human DNA sequence from clone RP4-799P18 on c
 complete sequence [Homo sapiens]
 Length = 144407

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Plus

Query: 18 gctgggaggaagacagg 34
 |||||
 Sbjct: 28804 gctgggaggaagacagg 28820

>[gi|9408716|emb|AL121980.14|HS1007G16](#) Human DNA sequence from clone RP5-1007G16 on c
 Contains part of the gene for a novel CUB and Sushi (SCR
 repeat) domain protein, a novel high-mobility group
 (nonhistone chromosomal) protein 2 (HMG2) like protein
 (pseudo) gene, a he>
 Length = 130604

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34
 |||||
 Sbjct: 6431 gctgggaggaagacagg 6415

>[gi|3366580|gb|AC004049.1|AC004049](#) Homo sapiens chromosome 4 clone B203C23 map 4q25,
 Length = 173766

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%)
 Strand = Plus / Plus

Query: 17 agctgggaggaagacag 33
 |||||
 Sbjct: 146187 agctgggaggaagacag 146203

>[gi|7228177|emb|AL133215.16|AL133215](#) Human DNA sequence from clone RP11-108L7 on chr
 part of the gene for a novel Insulin-like growth factor
 binding type protein with Kazal-type serine protease
 inhibitor domain, the gene for a novel protein similar to

rat tricarboxylat>
Length = 181086

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 19 ctgggaggaagacagga 35
|||||||
Sbjct: 55879 ctgggaggaagacagga 55895

>gi|57236|emb|X16362.1|RNSERPG Rat SPI-2 serine protease inhibitor gene
Length = 8005

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 23 gaggaagacaggaccct 39
|||||||
Sbjct: 4132 gaggaagacaggaccct 4148

>gi|8017427|emb|AJ289132.1|MMU289132 Mus musculus mRNA for chondroitin 4-O-sulfotran
Length = 1715

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagac 31
|||||||
Sbjct: 1216 gcagctgggaggaagac 1232

>gi|5420383|emb|AL034384.1|HSMTMO Human chromosome Xq28, cosmid clones 7H3, 14D7, C1
A12197, 12G8, A09100; complete sequence bases 1..217657
Length = 217657

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 22 ggaggaagacaggaccc 38
|||||||
Sbjct: 87105 ggaggaagacaggaccc 87121

>gi|1698996|gb|U78190.1|HSU78190 Human GTP cyclohydrolase I feedback regulatory prot
complete cds
Length = 4000

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 9 cgacgcgcagctgggag 25
|||||||
Sbjct: 371 cgacgcgcagctgggag 355

>gi|16549752|dbj|AK055096.1|AK055096 Homo sapiens cDNA FLJ30534 fis, clone BRAWH2001
Length = 2467

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 13 ggcgcagctgggaggaag 29
 |||||
Sbjct: 355 ggcgcagctgggaggaag 339

>gi|14588673|dbj|AP003492.2|AP003492 Oryza sativa genomic DNA, chromosome 1, PAC clo
 Length = 158084

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 3 cgaggccgacgcgcgac 19
 |||||
Sbjct: 144854 cgaggccgacgcgcgac 144838

>gi|14023393|dbj|AP003001.2|AP003001 Mesorhizobium loti DNA, complete genome, sectio
 Length = 345783

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 3 cgaggccgacgcgcgac 19
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Sbjct: 344778 cgaggccgacgcgcgac 344762

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences).

Posted date: Nov 14, 2001 1:05 AM

Number of letters in database: 60,694,059

Number of sequences in database: 1,020,477

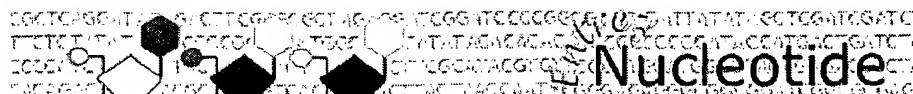
Lambda	K	H
1.37	0.711	1.31

Gapped Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 80,132
Number of Sequences: 1021646
Number of extensions: 80132
Number of successful extensions: 25674
Number of sequences better than 10.0: 54
length of query: 40
length of database: 4,680,328,494
effective HSP length: 18
effective length of query: 22
effective length of database: 4,661,938,866
effective search space: 102562655052
effective search space used: 102562655052
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)

S1: 12 (24.3 bits)
S2: 17 (34.2 bits)

5834183-7 Sequence alignment with 09/445614



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Book
Search	Nucleotide	for					Go	Clear
Limits		Preview/Index		History		Clipboard		Details
Display	GenBank	Save	Text	Add to Clipboard				

☐ 1: AF129112. Homo sapiens vani...[gi:4589140]

Related Sequences, Protein, PubMed, Taxonomy,
LinkOut

LOCUS AF129112 2397 bp mRNA PRI 20-APR-1999
DEFINITION Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA,
complete cds.
ACCESSION AF129112
VERSION AF129112.1 GI:4589140
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2397)
AUTHORS Caterina,M.J., Rosen,T.A., Tominaga,M., Brake,A.J. and Julius,D.
TITLE A capsaicin-receptor homologue with a high threshold for noxious
heat
JOURNAL Nature 398 (6726), 436-441 (1999)
MEDLINE 99215558
REFERENCE 2 (bases 1 to 2397)
AUTHORS Caterina,M.J., Rosen,T.A., Tominaga,M., Brake,A.J. and Julius,D.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1999) Cellular and Molecular Pharmacology,
University of California, 513 Parnassus, San Francisco, CA 94143,
USA
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Revised: October 24, 2001.

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